

WHAT IS CLAIMED IS:

1. A recombinant nucleic acid molecule comprising a heterologous promoter sequence operably linked to a nucleic acid sequence, wherein the promoter sequence comprises a transcriptional regulatory region capable of mediating seed-specific expression in *Arabidopsis* wherein the transcriptional regulatory region:
- is obtainable from a 5' region of a plant *FAEI* gene; or
 - hybridizes under stringent conditions to the 5' region of the plant *FAEI* gene; or
 - is at least 70% identical when optimally aligned to the 5' region of the plant *FAEI* gene.

2. The recombinant nucleic acid of claim 1 wherein the 5' region of the plant *FAEI* gene comprises (5' to 3'):

```

          AGA   TCTAAGAACA   CACATTCCCT   CAAATTTTAA   TGCACATGTA
ATCATAGTTT   AGCACAATTC   AAAAATAATG   TAGTATTAAA   GACAGAAATT
TGTAGACTTT   TTTTGGCGT   TAAAGGAAGA   CTAAGTTTAT   ACGTACATTT
TATTTTAAGT   GGAAAACCGA   AATTTTCCAT   CGAAATATAT   GAATTTAGTA
TATATATTTT   TGCAATGTAC   TATTTTGCTA   TTTTGGCAAC   TTTCAGTGGA
CTACTACTTT   ATTACAATGT   STATGGATGC   ATGAGTTTGA   GTATACACAT
GTCTAAATGC   ATGCTTTGCA   AAACGTAACG   GACCACAAAA   GAGGATCCAT
GCAAATACAT   CTCATAGCTT   CCTCCATTAT   TTTCCSACAC   AAACAGAGCA.

```

3. The recombinant nucleic acid of claim 1 wherein the 5' region of the plant *FAEI* gene comprises (5' to 3'):

```

AAGGCTTACC   CTATTAGTTG   AAAGTTGAAA   CTTTSTTCCC   TACTCAATTC
CTAGTTGTGT   AAATGTATGT   ATATGTAATG   CSTATAAAAC   CTAGTACTTA
AATGACTAGG   AGTGCTTCTT   GAGACCGATG   AGAGATGGGA   GAGAACTAA
AGATCATGAC   ATAATTAAGA   ACGAATTTGA   AAGGCTCTTA   GTTTTCAATC
CTATTCCAGA   ATGTTTTTGT   CAAAGATAST   GCGGATTTTG   AACCAAGAA
AACATTTAAA   AAATCAGTAT   CCGGTTACGT   TCATGCAAAAT   AGAAAGTGGT
CTAGGATCTG   ATTGTAATTT   TAGACTTAAA   GAGTCTCTTA   AGATTCAATC
CTGGCTGTGT   ACAAACTAC   AAATAATATA   TTTTAGACTA   TTTGGCCTTA
ACTAAACTTC   CACTCATTAT   TTAATGAGGT   TAGAGATATG   ACTTGCGAAT

```

AAACACATTC CCGAGAAATA CTCATGATCC CATAATTAGT CAGAGGGGTAT
 GCCAATCAGA TCTAAGAACA CACATTCCCT CAAATTTTAA TGCACATGTA
 ATCATAGTTT AGCACAATTC AAAAATAATG TAGTATTAAA GACAGAAATT
 TGTAGACTTT TTTTGGCGT TAAAGGAAGA CTAAGTTTAT ACGTACATTT
 5 TATTTTAAGT GGAAAACCGA AATTTTCCAT CGAAATATAT GAATTTAGTA
 TATATATTTG TGCAATGTAC TATTTTGCTA TTTTGGCAAC TTTCASTGGA
 CTACTACTTT ATTACAATGT GTATGGATGC ATGAGTTTGA GTATACACAT
 GTCTAAATGC ATGCTTTGCA AAACGTAAAG GACCACAAAA GAGGATCCAT
 GCAAATACAT CTCATAGCTT CCTCCATTAT TTTCCGACAC AAACAGAGCA.

10

4. The recombinant nucleic acid of claim 1 wherein the 5' region of the plant *FAE1* gene comprises (5' to 3'):

CTGACTTC ACCAAAGAAA CAACTCGAGT CGTTATCCAT
 CTCCTCATAA CCATCGCTCC ACTCTTTGSC TTCACCGTTT TCGGTTCCGT
 15 TCTCTACATC GCAACCCGGG CCAAACCGGT TTACCTCGTT GAGTACTCAT
 GCTACCTTCC ACCAACGCAT TGTAGATCAA GTATCTCCAA GGTGATGGAT
 ATCTTTTATC AAGTAAGAAA AGCTGATCCT TCTCGGAACG GCACGTGCGA
 TGACTCGTCC TGGCTTGACT TCTTGAGGAA GATTCAAGAA CGTTCAGGTC
 TAGGCGATGA AACTCACGGG CCGAGGGGGC TGCTTCAGGT CCTCCCGG
 20 AAGACTTTTG CGGCGGCGCG TGAAGAGAGG GAGCAAGTTA TCATTSGTGC
 GCTAGAAAAT CTATTCAAGA ACACCAACGT TAACCCTAAA GATATAGGTA
 TACTTGTGGT GAACTCAAGC ATSTTTAATC CAACTCCATC GGTCTCCGCG
 ATGGTGGTTA ACACCTTCOA SCTCCGAAGC AACGTAAGAA GCTTTAACCT
 TGGTGGCATG GCTTGTAGTG CCGGCTTAT AGCCATTGAT CTAGCAAAGG
 25 ACTTGTGGA TGTCCATAAA AATAGGTATG CTCTTGTGGT GAGCAGAGAG
 AACATCACTT ATAACATTTA CGCTGTTGAT AATAGSTCCA TGATGTTTTG
 AAATTTCTTG TTCCGTGTTG GTGGGGCCGC TATTTTGCTC TCCAACAAGC
 CTGGAGATCG TAGACGGTCC AAGTAGAGGC TAGTTCACAC GGTTCGAACG
 CATACCGGAG CTGACGACAA GTCTTTTCTG TCGGTGCAAC AAGGAGACGA
 30 TGAGAACGGG AAAATCGGAG TGAGTTTGTG CAAGGACATA ACCGATGTTG
 CTGGTGGAA CTTAAGAAA AACATAGCAA CGTTGGGTCC GTTGATTCTT
 CCGTTAAGCG AGAAACTTCT TTTTTCCTT ACCTTCATGG GCAAGAAACT
 TTTCAAGAT AAAATCAAGC ATTACTAGCT CCGGATTTG AAACCTTGCTA
 TTGACCATTT TTGTATACAT GCGGAGGGA GAGCGGTGAT TGATGTGCTA
 35 GAGAAGAACC TAGCCCTAGC ACCGATCGAT GTAGAGGCAT CAAGATCAAC
 GTTACATAGA TTTGGAAACA CTTCATCTAG CTCAATATGG TATGAGTTGG

5
 10
 15
 20
 25
 30

CATACATAGA AGCAAAAGGA AGGATGAAGA AAGGTAAATA AGTTTGGCAG
 ATTGCTTTAG GGTGAGGCTT TAAGTGTAAC AGTGCAGTTT GGGTGGCTCT
 AAACAATGTC AAAGCTTCGA CAAATAGTCC TTGGGAACAC TGCATCGACA
 GATACCCGGT CAAAATTGAT TCTGATTGAG GTAAGTCAGA GACTCGTGTC
 CAAAACGGTC GGTCCTAATA AACGATGTTT GCTCTCTTTC GTTTCTTTTT
 ATTTGTTATA ATAATTTGAT GGCTACGATG TTTCTCTTGT TTGTTATGAA
 TAAAGAATGC AATGGTGTTG TAGTATTTGA TTGTTTTACA TGTATGATC
 TCTTATTTAC ATGAAATTTT TAAACGCCA AAAAAAAAAA CGGAATTCG.

- 10 5. The recombinant nucleic acid of claim 1 wherein the 5' region of the plant *FAE1* gene comprises (5' to 3'):

15
 20
 25
 30

CAGCTTAAC CGGTAAAATT
 GGCCTGTACA TATATTTACC ACTGAGTAAA GACATCAGTT AATGATTTGT
 TGTACTCAA TTGGGCTAAG TGTATTATTA TATGTSTTGT ATATAATAAA
 GGTAGAACGT AAATTTACTA AGAATGTGTT TTTCCAATGT GATTGCTCTT
 TGGCCTCTTA GTTTTGAATC CTACTCGAGA AGACTAATTT TAATTTACTG
 GCAAAAATAG AAATCAATTT ATAAGTGTTT AAACAAATCG ATGGTATAAC
 TGATTAGTGA TCACTCTTAG GTTTTGATCC AACTCGAGTA TTCAGTATTG
 AACGCTTTTT TTAAATAAAA TCTTGATTTT TAAATTGGTT TTTTGAGTAA
 AAAAGTTCTT AATATTTTCT CTTTGTTTTA ATGGGTTTGT TTTGCATTTT
 ATAAGCTTAA TTTTCTAAT TTAATATTTT ATCTATCATC GTCCGTAAAG
 TTTTATTTGG CACAAACTTG TTTTACTTTT CTACCTTATA ATTTGGGAAC
 TGGTTGAGTC AAAGCGTACC GGACAAATAT GTTTTATATT CTTATTTAAG
 AATTAACACT CATCTCATTA TTAGTCAGAG GGTAGGGAGA TTCAGCCAAT
 CAATGCTAAC AACAAAATTC TCTTAATGAT CTAACGATGC TATTTAATAT
 TCGGATCAGT ATTCTTAAAT AAGAATATAA AACTAATTCA ATAGTTACAG
 ATAAAAACTT ATATAGACTT TTTTATTTGG AATATAAAAG TATCAATATA
 TTATAGACAA TATTTATAAC GTTAAAAATA CAATATTTAT ATTTTATATA
 TATTTATTTG AAATTGAAAA GCATTACTTC TATCGAAATG AATTTTAGTA
 TATTAATTAA TATTTTTTTA ATCGGACTAC TTTCTATTTT TGGCACCTTT
 CATCTGACTA CTAATTTTAT TCAATGTGTA TGCATGCATG AGCATCAGTA
 ATACACATGT CTATATAAAT GCATGTAAAA CATAACGGAC CACAAAAGTG
 GATCCATAGA AATACATCTC ATCGGACCTT CTCCGACACA AAATGAGCA.

6. The recombinant nucleic acid of claim 1 wherein the promoter sequence is selected from the group consisting of *Arabidopsis thaliana*, *Lunaria annua* and *Brassica napus* *FAE1* promoter sequences.
- 5 7. The recombinant nucleic acid of any one of claims 1 through 6, wherein the transcriptional regulatory region is at least 70% identical when optimally aligned to the 5' region of the plant *FAE1* gene..
8. The recombinant nucleic acid of claim 1 wherein the transcriptional regulatory region comprises (5' to 3'):
- 10
- | | | | | | |
|----|-------------|------------|------------|------------|-------------|
| | AGA | TCTAAGAACA | CACATTCCCT | CAAATTTTAA | TGCACATGTA |
| | ATCATAGTTT | AGCACAATTC | AAAAATAATG | TAGTATTAAA | GACAGAAATT |
| | TGTAGACTTT | TTTTTGGCGT | TAAAGGAAGA | CTAAGTTTAT | ACGTACATTT |
| | TATTTTAAAGT | GGAAAACCGA | AATTTTCCAT | CGAAATATAT | GAATTTAGTA |
| 15 | TATATATTTT | TGCAATGTAC | TATTTTGCTA | TTTTGGCAAC | TTTCAGTGGA |
| | CTACTACTTT | ATTACAATGT | GTATGGATGC | ATGAGTTTGA | GTATACACAT |
| | GTCTAAATGC | ATGCTTTGCA | AAACGTAACG | GACCACAAAA | GAGGATCCAT |
| | GCAATACAT | CTCATAGCTT | CCTCCATTAT | TTCCGACAC | AAACAGAGCA. |
- 20
9. The recombinant nucleic acid of claim 1 wherein the transcriptional regulatory region comprises (5' to 3'):
- 25
- | | | | | | |
|----|------------|-------------|------------|-------------|------------|
| | AAGGCTTACC | CTATTAGTTG | AAAGTTGAAA | CTTTGTTCCC | TACTCAATTC |
| | CTAGTTGTGT | AAATGTATGT | ATATGTAATG | CCTATAAAAC | CTAGTACTTA |
| 25 | AATGACTAGG | AGTGGTTCTT | GAGACCGATG | AGAGATGGGA | GCAGAACTAA |
| | AGATGATGAC | ATAATTAAGA | ACGAATTGGA | AAGGCTCTTA | GGTTTGAATC |
| | CTATTCGAGA | ATGTTTTTST | CAAAGATAST | GGCGATTTTG | AACCAAAGAA |
| | AACHTTTTAA | AAATCAGTAT | CCGTTTACGT | TCATGCAAAAT | AGAAAGTSGT |
| | CTAGGATCTG | ATTGTAATTT | TAGACTTAAA | GAGTCTCTTA | AGATTCAATC |
| 30 | CTGGCTGTGT | ACAAAACCTAC | AAATAATATA | TTTTAGACTA | TTTGGCCTTA |
| | ACTAAACTTC | CAGTCATTAT | TACTSAGST | TAGAGAATAG | ACTTSCGAAT |
| | AAACACATTC | CCGAGAAATA | CTCATGATCC | CATAATTAGT | CAGAGGGTAT |
| | GCCAATCAGA | TCTAAGAACA | CACATTCCCT | CAAATTTTAA | TGCACATGTA |
| | ATCATAGTTT | AGCACAATTC | AAAAATAATG | TAGTATTAAA | GACAGAAATT |
| 35 | TGTAGACTTT | TTTTTGGCGT | TAAAGGAAGA | CTAAGTTTAT | ACGTACATTT |

TATTTTAAGT CGAAAACCGA AATTTTCCAT CGAAATATAT GAATTTAGTA
 TATATATTTT TGCAATGTAC TATTTTGCTA TTTTGGCAAC TTTCAGTGGA
 CTAATACTTT ATTACAATGT GTATGGATGC ATGAGTTTGA GTATACACAT
 GTCTAAATGC ATGCTTTTGA AAACGTAACG GACCACAAAA GAGGATCCAT
 5 GCAAATACAT CTCATAGCTT CCTCCATTAT TTTCCGACAC AAACAGAGCA.

10. The recombinant nucleic acid of claim 1 wherein the transcriptional regulatory region comprises (5' to 3'):

10

CTGACTTC ACCAAAGAAA CAACTCGAGT CGTTATCCAT
 CTCCTCATAA CCATCGCTCC ACTCTTTGCC TTCACCGTTT TCGGTTCCGGT
 TCTCTACATC GCAACCCGGC CCAAACCGGT TTACCTCGTT GAGTACTCAT
 GCTACCTTCC ACCAACGCAT TGTAGATCAA GTATCTCCAA GGTATGGAT
 15 ATCTTTTATC AAGTAAGAAA AGCTGATCCT TCTCGGAACG GCACGTGCGA
 TGACTCGTCC TGGCTTGACT TCTTGAGGAA GATTCAAGAA CGTTCAGGTC
 TAGGCGATGA AACTCACGGG CCGGAGGGGC TGCTTCAGGT CCGTCCCGGG
 AAGACTTTTG CGGCGGGCGG TGAAGAGACG GAGCAAGTTA TCATTGGTGC
 GCTAGAAAAT CTATTCAAGA ACACCAACGT TAACCTAAA GATATAGGTA
 20 TACTTGTGGT GAACTCAAGC ATGTTTAATC CAACTCCATC GCTCTCCGCG
 ATGGTCTGTTA AACTTTTCAA GCTCCGAAGC AACGTAAGAA GCTTTAACCT
 TGGTGGCATG GGTGTAGTGC CCGGCGTTAT AGCCATTGAT CTAGCAAAGG
 ACTTGTTCGA TGTCCATAAA AATACGTATG CTCTTGTGGT GAGCACAGAG
 AACATCACTT ATAACATTTA CGCTGCTGAT AATAGCTCCA TCATGCTTTC
 25 AAATTGCTTC TTCCGTGTTG GTGGGGGGGG TATTTTCTTC TCCAAACAGC
 CTGGAGATCC TAGACGCTCC AAGTACGAGC TAGTTCACAC GGTTCGAAGC
 CATACCGGAG CTGACGACAA GTCTTTTCGT TCGTSCAAC AAGGAGACGA
 TGAGAACGGC AAAATCGGAG TSAGTTTGTC CAAGGACATA ACCGATGTTG
 CTGGTCCGAC GGTTAAGAAA AACATAGCAA CGTTGGGTCC GTTGATTCTT
 30 CCGTTAAGCG AGAACTTCT TTTTTCGTT ACCTTCATGC GCAAGAAACT
 TTTCAAAGAT AAAATCAAC ATTACTACGT CCGGATTTC AAACCTCCTA
 TTGACCATTT TTGTATACAT CCGGAGGCA GAGCCGTCAT TCATGTGCTA
 GAGAAGAAGC TAGCCCTAGC ACCGATGAT CTAGAGGCAT CAAGATCAAC
 GTTACATAGA TTTGGAACA GTTCATCTAG CTCAATATGG TATGAGTTGG
 35 CATACATAGA AGCAAAAGGA AGGATGAAGA AAGGTAATAA AGTTTGGCAG
 ATTGCTTTAG GGTGAGGCTT TAAGTCTAAC AGTGCAGTTT GGGTGGCTCT
 AAACAATGTC AAAGCTTCCA CAAATAGTCC TTGGGAACAC TGCATCGACA

GATACCCGGT CAAAATTGAT TGTGATTCAG GTAAGTCAGA GACTCGTGTG
 CAAAACGGTC GGTCCATAA AACGATGTTT GGTCTCTTTC GTTCTTTTTT
 ATTTGTTATA ATAATTTGAT GGCTACGATG TTTCTCTTGT TTGTTATGAA
 TAAAGAATGC AATGGTGTTT TAGTATTTGA TTGTTTTACA TGTATGTATC
 5 TGTATTTTAC ATGAAATTTT TAAACGCCTA AAAAAAAAAA CGGAATTCGG.

11. The recombinant nucleic acid of claim 1 wherein the transcriptional regulatory region comprises (5' to 3'):

10 CAGCTTAAC CGGTAAAATT
 GGCCTGTACA TATATTTACC ACTGAGTAAA GACATCAGTT AATGATTTGT
 TGTACTCAA TTGGGCTAAG TGTATTATTA TATGTGTTGT ATATAATPAA
 GGTAGAACGT AAATTTACTA AGAATGTGTT TTTCCAATGT GATTGCTCTT
 15 TGGCCTCTTA GGTTTGAATC CTACTCGAGA AGACTAATTT TAATTTACTG
 SCAAAAATAG AAATCAATTT ATAAGTGTTC AACCAATCG ATGGTATAAC
 TGATTAGTGA TCACTCTTAG GTTTTGATCC AACTCGAGTA TTGAGTATTG
 AACGCTTTTT TTAATAAAAA TCTTGATTTT TAAATTGGTT TTTTGAGTAA
 AAAAGTTCTT AATATTTTCT CTTTGTTTTA ATGGGTTTGT TTTGCATTTT
 20 ATAAGCTTAA TTTTCTAAT TTAATATTTT ATCTATCATC GTCCGTAAAG
 TTTTATTTGG CACAAACTTG TTTTACTTTT CTACCTTATA ATTTGGGAAC
 TGGTTGAGTC AAAGCGTACC GGACAATAT GTTTTATATT CTTATTTAAG
 AATTAACACT CATCTCATAA TTAGTCAGAG GCTAGGGAGA TTCAGCCAAT
 CAATGCTAAC AACAAAATTC TCTTAATGAT CTAACGATGC TATTTAATAT
 25 TCGGATCAAT ATTCTTAAT AGAATATTA ACTAATTC AATAGTTACAG
 ATAAAAACTT ATATAGACTT TTTTATTTGG AATATAAAG TATCAATATA
 TTATAGACAA TATTTATAAC GTTAAAAATA CAATATTTAT ATTTTATATA
 TATTTATTTT AAATTGAAAA GCATTACTTC TATCGAAATG AATTTTAGTA
 TATTAATTAA TATTTTTTTA ATCGGACTAC TTTCTATTTT TGGCACCTTT
 30 CATCTGACTA CTAATTTATT TCAATGTGTA TGCATGCATG AGCATSAGTA
 ATACACATGT CTATATAAAT GCATGTAAAA CTAACGGAC CACAAAAGTG
 GATCCATAGA AATACATCTC ATCGCACCTT CTCGGACACA AAACCTGAACA.

12. The recombinant nucleic acid of any one of claims 1 through 11 wherein the nucleic acid sequence encodes a translatable mRNA.

13. The recombinant nucleic acid of claim 12 wherein the nucleic acid sequence encodes an enzyme involved in lipid metabolism.
14. The recombinant nucleic acid of any one of claims 1 through 13, further comprising a transcription termination region operably linked to the nucleic acid sequence.
15. A host cell comprising the recombinant nucleic acid of any one of claims 1 through 14.
16. The host cell of claim 15, wherein the host cell is of a dicotyledonous plant species.
17. A plant comprising the recombinant nucleic acid of any one of claims 1 through 14.
18. The plant of claim 17, wherein the plant is of a dicotyledonous plant species.
19. A method of altering the phenotype of a seed comprising:
- a) transforming a seed-bearing plant, or a progenitor of the seed-bearing plant, with a vector comprising the nucleic acid of any one of claims 1 through 14;
 - b) growing the seed-bearing plant to obtain seed under conditions wherein the nucleic acid sequence is expressed during embryogenesis under the control of the transcriptional regulatory region to alter the phenotype of the seed.
20. A method of transforming a plant cell comprising transforming the plant cell with the recombinant nucleic acid of any one of claims 1 through 14.